



OIEP

## RAW SEQUENCE LISTING

DATE: 07/23/2002

PATENT APPLICATION: US/10/098,602A

TIME: 14:33:23

Input Set : A:\12557-004001.txt

Output Set: N:\CRF3\07232002\J098602A.raw

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4 <110> APPLICANT: Kloek, Andrew P.
5      Williams, Deryck Jeremy
6      Salmon, Brandy
8 <120> TITLE OF INVENTION: NEMATODE GS-LIKE SEQUENCES
10 <130> FILE REFERENCE: 12557-004001
12 <140> CURRENT APPLICATION NUMBER: US 10/098,602A
13 <141> CURRENT FILING DATE: 2002-03-15
15 <150> PRIOR APPLICATION NUMBER: US 60/276,621
16 <151> PRIOR FILING DATE: 2001-03-16
18 <160> NUMBER OF SEQ ID NOS: 9
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1471
24 <212> TYPE: DNA
25 <213> ORGANISM: Meloidogyne incognita
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (34)...(1395)
31 <400> SEQUENCE: 1
32 tgtataataa agcttcataa tataaaattt taa atg acc atc act tat gat gaa      54
33                               Met Thr Ile Thr Tyr Asp Glu
34                               1           5
36 cta aat aat ttg att aga aat gga aaa att gac acg gta gtt ttg gca      102
37 Leu Asn Asn Leu Ile Arg Asn Gly Lys Ile Asp Thr Val Val Leu Ala
38      10           15           20
40 tgc gtc gac atg caa ggc cgg ctg atg ggc aag aga tta act ggg cgt      150
41 Cys Val Asp Met Gln Gly Arg Leu Met Gly Lys Arg Leu Thr Gly Arg
42      25           30           35
44 cat ttt tta gga ttg gat caa aag aag att agc att agc acg ttt gta      198
45 His Phe Leu Gly Leu Asp Gln Lys Lys Ile Ser Ile Ser Thr Phe Val
46 40           45           50           55
48 tat gcg gta act ata gaa ggc atc gct ggc gga ggt tat gag atc tca      246
49 Tyr Ala Val Thr Ile Glu Gly Ile Ala Gly Gly Gly Tyr Glu Ile Ser
50      60           65           70
52 agt gta gac aca ggt tat agt gat tgt cat ctc tgt gca gat ttg aat      294
53 Ser Val Asp Thr Gly Tyr Ser Asp Cys His Leu Cys Ala Asp Leu Asn
54      75           80           85
56 tcc ctt cat tta ctc ccg tgg tca gaa ggc gct gta ttg gca att tcc      342
57 Ser Leu His Leu Leu Pro Trp Ser Glu Gly Ala Val Leu Ala Ile Ser
58      90           95           100
60 aat cct cat aat ttc gtt act tct gag cca ttg ttc tgt tct cct cga      390
61 Asn Pro His Asn Phe Val Thr Ser Glu Pro Leu Phe Cys Ser Pro Arg
62      105           110           115

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64	gta	ata	ctc	atg	cag	caa	att	gag	cgc	ctg	gct	aat	cta	aag	ctt	aaa	438
65	Val	Ile	Leu	Met	Gln	Gln	Ile	Glu	Arg	Leu	Ala	Asn	Leu	Lys	Leu	Lys	
66	120				125					130						135	
68	ggc	ctt	ttt	gct	tct	gaa	cta	gaa	ttt	aat	ctt	ttc	aac	gaa	act	tat	486
69	Gly	Leu	Phe	Ala	Ser	Glu	Leu	Glu	Phe	Asn	Leu	Phe	Asn	Glu	Thr	Tyr	
70				140					145						150		
72	aag	agt	gcc	agc	caa	aag	cat	tgg	aaa	aat	tta	aaa	acc	gcg	cag	cct	534
73	Lys	Ser	Ala	Ser	Gln	Lys	His	Trp	Lys	Asn	Leu	Lys	Thr	Ala	Gln	Pro	
74				155					160					165			
76	cat	cat	caa	tgg	atg	aat	att	agt	gca	agt	agt	ggg	att	gaa	act	ttt	582
77	His	His	Gln	Trp	Met	Asn	Ile	Ser	Ala	Ser	Ser	Gly	Ile	Glu	Thr	Phe	
78			170					175					180				
80	atg	cgt	tct	gtg	cgt	aat	aaa	tta	gaa	gaa	gcc	ggt	att	ttg	atg	gag	630
81	Met	Arg	Ser	Val	Arg	Asn	Lys	Leu	Glu	Glu	Ala	Gly	Ile	Leu	Met	Glu	
82	185				190					195							
84	gcg	aca	cat	ccc	gaa	ttt	tta	cct	agt	cag	cat	gaa	ctt	aat	ttt	gta	678
85	Ala	Thr	His	Pro	Glu	Phe	Leu	Pro	Ser	Gln	His	Glu	Leu	Asn	Phe	Val	
86	200				205				210						215		
88	cca	gcc	gat	cct	cta	aca	atg	gca	gat	cgt	cat	att	att	gca	aaa	cat	726
89	Pro	Ala	Asp	Pro	Leu	Thr	Met	Ala	Asp	Arg	His	Ile	Ile	Ala	Lys	His	
90				220					225					230			
92	gga	gtt	cgc	gaa	atg	gca	gaa	cag	tct	gga	atg	gtt	gca	act	ttt	atg	774
93	Gly	Val	Arg	Glu	Met	Ala	Glu	Gln	Ser	Gly	Met	Val	Ala	Thr	Phe	Met	
94			235					240					245				
96	gct	aaa	ttg	agt	tca	act	gcg	ctt	ggt	aat	gcc	tgc	cat	att	cat	atg	822
97	Ala	Lys	Leu	Ser	Ser	Thr	Ala	Leu	Gly	Asn	Ala	Cys	His	Ile	His	Met	
98			250					255				260					
100	tca	ctt	caa	gat	gca	gaa	aca	gaa	aaa	aat	gca	ttt	tat	gat	caa	aac	870
101	Ser	Leu	Gln	Asp	Ala	Glu	Thr	Glu	Lys	Asn	Ala	Phe	Tyr	Asp	Gln	Asn	
102			265				270					275					
104	gat	gaa	tat	gga	atg	tca	acc	tta	gct	cgt	aat	tgg	att	gct	gga	tta	918
105	Asp	Glu	Tyr	Gly	Met	Ser	Thr	Leu	Ala	Arg	Asn	Trp	Ile	Ala	Gly	Leu	
106	280				285					290					295		
108	ttg	aaa	tac	gta	cct	gaa	gcg	act	tat	ttc	ttt	gca	tct	tac	atc	aac	966
109	Leu	Lys	Tyr	Val	Pro	Glu	Ala	Thr	Tyr	Phe	Phe	Ala	Ser	Tyr	Ile	Asn	
110				300					305					310			
112	tcg	tac	aaa	aga	ctt	caa	ccg	ctt	act	ttt	gcg	cca	aca	aaa	tgt	tgt	1014
113	Ser	Tyr	Lys	Arg	Leu	Gln	Pro	Leu	Thr	Phe	Ala	Pro	Thr	Lys	Cys	Cys	
114				315					320					325			
116	tgg	gca	att	gac	aac	cga	aca	agc	gcc	ttt	cga	ctt	tgt	aat	tca	aaa	1062
117	Trp	Ala	Ile	Asp	Asn	Arg	Thr	Ser	Ala	Phe	Arg	Leu	Cys	Asn	Ser	Lys	
118			330					335					340				
120	tcc	gag	gga	att	aat	gtt	gag	ctg	cgt	att	ggt	ggc	gct	gat	ttg	aac	1110
121	Ser	Glu	Gly	Ile	Asn	Val	Glu	Leu	Arg	Ile	Gly	Gly	Ala	Asp	Leu	Asn	
122			345				350					355					
124	cct	tat	tta	gct	ttt	tcc	gca	atc	ata	gct	gca	gga	att	agc	ggt	ata	1158
125	Pro	Tyr	Leu	Ala	Phe	Ser	Ala	Ile	Ile	Ala	Ala	Gly	Ile	Ser	Gly	Ile	
126	360				365					370				375			
128	gaa	gaa	aag	ctt	gaa	ctt	ccc	cct	cct	gca	tct	ggc	aat	gtt	tac	aat	1206

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129 Glu Glu Lys Leu Glu Leu Pro Pro Pro Ala Ser Gly Asn Val Tyr Asn
130          380          385          390
132 gat aag gaa tta cct gaa ttt cct aat tcc tta caa aat gct aca cat      1254
133 Asp Lys Glu Leu Pro Glu Phe Pro Asn Ser Leu Gln Asn Ala Thr His
134          395          400          405
136 ctt cta aaa gaa tcg aaa atg ctg aat aaa aca ttc ggg gag aag ttg      1302
137 Leu Leu Lys Glu Ser Lys Met Leu Asn Lys Thr Phe Gly Glu Lys Leu
138          410          415          420
140 att cta cat tat gta aac gct gct aat gtt gag att aat gaa ttt tca      1350
141 Ile Leu His Tyr Val Asn Ala Ala Asn Val Glu Ile Asn Glu Phe Ser
142          425          430          435
144 aaa caa gtt act gac tgg gag ctt aat caa gga ttt aat aga tat      1395
145 Lys Gln Val Thr Asp Trp Glu Leu Asn Gln Gly Phe Asn Arg Tyr
146 440          445          450
148 taatatattta atgcttatgt agataacaat caaaaatata atctttaaat acataattaa      1455
149 aaaaaaaaaa aaaaaa      1471
151 <210> SEQ ID NO: 2
152 <211> LENGTH: 454
153 <212> TYPE: PRT
154 <213> ORGANISM: Meloidogyne incognita
156 <400> SEQUENCE: 2
157 Met Thr Ile Thr Tyr Asp Glu Leu Asn Asn Leu Ile Arg Asn Gly Lys
158 1          5          10          15
159 Ile Asp Thr Val Val Leu Ala Cys Val Asp Met Gln Gly Arg Leu Met
160          20          25          30
161 Gly Lys Arg Leu Thr Gly Arg His Phe Leu Gly Leu Asp Gln Lys Lys
162          35          40          45
163 Ile Ser Ile Ser Thr Phe Val Tyr Ala Val Thr Ile Glu Gly Ile Ala
164          50          55          60
165 Gly Gly Gly Tyr Glu Ile Ser Ser Val Asp Thr Gly Tyr Ser Asp Cys
166 65          70          75          80
167 His Leu Cys Ala Asp Leu Asn Ser Leu His Leu Leu Pro Trp Ser Glu
168          85          90          95
169 Gly Ala Val Leu Ala Ile Ser Asn Pro His Asn Phe Val Thr Ser Glu
170          100          105          110
171 Pro Leu Phe Cys Ser Pro Arg Val Ile Leu Met Gln Gln Ile Glu Arg
172          115          120          125
173 Leu Ala Asn Leu Lys Leu Lys Gly Leu Phe Ala Ser Glu Leu Glu Phe
174          130          135          140
175 Asn Leu Phe Asn Glu Thr Tyr Lys Ser Ala Ser Gln Lys His Trp Lys
176 145          150          155          160
177 Asn Leu Lys Thr Ala Gln Pro His His Gln Trp Met Asn Ile Ser Ala
178          165          170          175
179 Ser Ser Gly Ile Glu Thr Phe Met Arg Ser Val Arg Asn Lys Leu Glu
180          180          185          190
181 Glu Ala Gly Ile Leu Met Glu Ala Thr His Pro Glu Phe Leu Pro Ser
182          195          200          205
183 Gln His Glu Leu Asn Phe Val Pro Ala Asp Pro Leu Thr Met Ala Asp
184          210          215          220

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```

185 Arg His Ile Ile Ala Lys His Gly Val Arg Glu Met Ala Glu Gln Ser
186 225                230                235                240
187 Gly Met Val Ala Thr Phe Met Ala Lys Leu Ser Ser Thr Ala Leu Gly
188                245                250                255
189 Asn Ala Cys His Ile His Met Ser Leu Gln Asp Ala Glu Thr Glu Lys
190                260                265                270
191 Asn Ala Phe Tyr Asp Gln Asn Asp Glu Tyr Gly Met Ser Thr Leu Ala
192                275                280                285
193 Arg Asn Trp Ile Ala Gly Leu Leu Lys Tyr Val Pro Glu Ala Thr Tyr
194                290                295                300
195 Phe Phe Ala Ser Tyr Ile Asn Ser Tyr Lys Arg Leu Gln Pro Leu Thr
196 305                310                315                320
197 Phe Ala Pro Thr Lys Cys Cys Trp Ala Ile Asp Asn Arg Thr Ser Ala
198                325                330                335
199 Phe Arg Leu Cys Asn Ser Lys Ser Glu Gly Ile Asn Val Glu Leu Arg
200                340                345                350
201 Ile Gly Gly Ala Asp Leu Asn Pro Tyr Leu Ala Phe Ser Ala Ile Ile
202                355                360                365
203 Ala Ala Gly Ile Ser Gly Ile Glu Glu Lys Leu Glu Leu Pro Pro Pro
204                370                375                380
205 Ala Ser Gly Asn Val Tyr Asn Asp Lys Glu Leu Pro Glu Phe Pro Asn
206 385                390                395                400
207 Ser Leu Gln Asn Ala Thr His Leu Leu Lys Glu Ser Lys Met Leu Asn
208                405                410                415
209 Lys Thr Phe Gly Glu Lys Leu Ile Leu His Tyr Val Asn Ala Ala Asn
210                420                425                430
211 Val Glu Ile Asn Glu Phe Ser Lys Gln Val Thr Asp Trp Glu Leu Asn
212                435                440                445
213 Gln Gly Phe Asn Arg Tyr
214                450

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216 &lt;210&gt; SEQ ID NO: 3

217 &lt;211&gt; LENGTH: 1362

218 &lt;212&gt; TYPE: DNA

219 &lt;213&gt; ORGANISM: Meloidogyne incognita

221 &lt;400&gt; SEQUENCE: 3

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222 atgaccatca cttatgatga actaaataat ttgattagaa atggaaaaat tgacacggta      60
223 gttttggcat gcgtcgacat gcaaggccgg ctgatgggca agagattaac tgggcgcat      120
224 tttttaggat tggatcaaaa gaagattagc attagcacgt ttgtatatgc ggtaactata      180
225 gaaggcatcg ctggcggagg ttatgagatc tcaagtgtag acacagggtta tagtgattgt      240
226 catctctgtg cagatttgaa ttcccttcat ttactcccg gtgcagaagg cgctgtattg      300
227 gcaatttcca atcctcataa ttctgttact tctgagccat tgttctgttc tcctcgagta      360
228 atactcatgc agcaaattga gcgcctggct aatctaaagc ttaaaggcct ttttgcttct      420
229 gaactagaat ttaatctttt caacgaaact tataagagtg ccagccaaaa gcattggaaa      480
230 aatttaaaaa cgcgcagccc tcatcatcaa tggatgaata ttagtgcaag tagtgggatt      540
231 gaaaactttta tgcgttctgt gcgtaataaa ttagaagaag ccggtatttt gatggaggcg      600
232 acacatcccg aatttttacc tagtcagcat gaacttaatt ttgtaccagc cgatcctcta      660
233 acaatggcag atcgtcatat tattgcaaaa catggagttc gcgaaatggc agaacagtct      720
234 ggaatggttg caacttttat ggctaaattg agttcaactg cgcttggtaa tgcttgcctat      780
235 attcatatgt cacttcaaga tgcagaaaca gaaaaaatg cattttatga tcaaacgat      840

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236 gaatatggaa tgtcaacctt agctcgtaat tggattgctg gattattgaa atacgtacct 900
237 gaagcgactt atttctttgc atcttacatc aactcgtaca aaagacttca accgcttact 960
238 ttgcgccaa caaatgttg ttgggcaatt gacaaccgaa caagcgctt tcgactttgt 1020
239 aattcaaaat ccgaggggaat taatgttgag ctgctgattg gtggcgctga tttgaacct 1080
240 tatttagctt ttccgcgaat catagctgca ggaattagcg gtatagaaga aaagcttgaa 1140
241 ctccccctc ctgcatctgg caatgtttac aatgataagg aattacctga atttcctaat 1200
242 tccttacaaa atgctacaca tcttctaaaa gaatcgaaaa tgctgaataa aacattcggg 1260
243 gagaagttga ttctacatta tgtaaacgct gctaattgtg agattaatga attttcaaaa 1320
244 caagttactg actgggagct taatcaagga tttaatatag at 1362
246 <210> SEQ ID NO: 4
247 <211> LENGTH: 457
248 <212> TYPE: PRT
249 <213> ORGANISM: Mycobacterium tuberculosis
251 <400> SEQUENCE: 4
252 Met Thr Gly Pro Gly Ser Pro Pro Leu Ala Trp Thr Glu Leu Glu Arg
253 1 5 10 15
254 Leu Val Ala Ala Gly Asp Val Asp Thr Val Ile Val Ala Phe Thr Asp
255 20 25 30
256 Met Gln Gly Arg Leu Ala Gly Lys Arg Ile Ser Gly Arg His Phe Val
257 35 40 45
258 Asp Asp Ile Ala Thr Arg Gly Val Glu Cys Cys Ser Tyr Leu Leu Ala
259 50 55 60
260 Val Asp Val Asp Leu Asn Thr Val Pro Gly Tyr Ala Met Ala Ser Trp
261 65 70 75 80
262 Asp Thr Gly Tyr Gly Asp Met Val Met Thr Pro Asp Leu Ser Thr Leu
263 85 90 95
264 Arg Leu Ile Pro Trp Leu Pro Gly Thr Ala Leu Val Ile Ala Asp Leu
265 100 105 110
266 Val Trp Ala Asp Gly Ser Glu Val Ala Val Ser Pro Arg Ser Ile Leu
267 115 120 125
268 Arg Arg Gln Leu Asp Arg Leu Lys Ala Arg Gly Leu Val Ala Asp Val
269 130 135 140
270 Ala Thr Glu Leu Glu Phe Ile Val Phe Asp Gln Pro Tyr Arg Gln Ala
271 145 150 155 160
272 Trp Ala Ser Gly Tyr Arg Gly Leu Thr Pro Ala Ser Asp Tyr Asn Ile
273 165 170 175
274 Asp Tyr Ala Ile Leu Ala Ser Ser Arg Met Glu Pro Leu Leu Arg Asp
275 180 185 190
276 Ile Arg Leu Gly Met Ala Gly Ala Gly Leu Arg Phe Glu Ala Val Lys
277 195 200 205
278 Gly Glu Cys Asn Met Gly Gln Glu Ile Gly Phe Arg Tyr Asp Glu
279 210 215 220
280 Ala Leu Val Thr Cys Asp Asn His Ala Ile Tyr Lys Asn Gly Ala Lys
281 225 230 235 240
282 Glu Ile Ala Asp Gln His Gly Lys Ser Leu Thr Phe Met Ala Lys Tyr
283 245 250 255
284 Asp Glu Arg Glu Gly Asn Ser Cys His Ile His Val Ser Leu Arg Gly
285 260 265 270
286 Thr Asp Gly Ser Ala Val Phe Ala Asp Ser Asn Gly Pro His Gly Met

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VERIFICATION SUMMARY

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Input Set : A:\12557-004001.txt

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